

SEQUENCE LISTING

<110> Ecole Polytechnique Fédérale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter protein

<130> PEPF001WO

<150> US 34,404 JM-213

<151> 2003-10-09

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 672

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> modified_base

<222> (186)..(186)

<223> silent point mutation introduced to generate HindIII restriction site

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 1

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atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgtag 60
agcacagagg cgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
gtgcccataa gaaagagaac aattgaccog gttattgcaa ggaaaatttc aagtcttgta 180
aaagcatata aaaatagttc aggcaactcg aaatacttgg ttggcgtggt tcgtaatcaa 240
cctaaggagg atgttttggc tctgggtcaat gattaaggca ttgatatcgt ccaactgcac 300
ggagatgagt cgtggcaaga ataccaagag ttctcgggtt tgccagttat taaaagactc 360
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctggtgga 540
ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600
agcggaggtg tggagacaaa tgggtgtaaaa gactctaaca aaatagcaaa tttcgtcaaa 660
aatgctaaga aa 672

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<210> 2

<211> 224

<212> PRT

<213> *Saccharomyces cerevisiae*

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 2

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Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1           5           10           15

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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20           25           30

```

```

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35           40           45

```

```

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50           55           60

```

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly
195 200 205

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
210 215 220

<210> 3

<211> 132

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> modified_base

<222> (22)..(22)

<223> point mutation

<400> 3

atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgacag 60
 agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
 gtgccaata ga 132

<210> 4

<211> 44

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
 35 40

<210> 5

<211> 540

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 5

aagagaacaa ttgaccoggt tattgcaagg aaaatttcaa gtcttgtaaa agcatataaa 60
 aatagttcag gcaactccgaa ataacttggtt ggcgtgtttc gtaatcaacc taaggaggat 120
 gttttggctc tggatcaatga ttacggcatt gatatcgtcc aactgcacgg agatgagtcg 180
 tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa 240
 gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt 300
 gattcagaag caggtgggac aggtgaactt ttggattgga actcgatttc tgactggggt 360
 ggaaggcaag agagccccga gagcttacat tttatgttag ctggtggact gacgccagaa 420
 aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg 480
 gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtcaaaaa tgctaagaaa 540

<210> 6

<211> 180

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 6

Lys	Arg	Thr	Ile	Asp	Pro	Val	Ile	Ala	Arg	Lys	Ile	Ser	Ser	Leu	Val
1				5					10					15	

Lys	Ala	Tyr	Lys	Asn	Ser	Ser	Gly	Thr	Pro	Lys	Tyr	Leu	Val	Gly	Val
			20					25					30		

Phe	Arg	Asn	Gln	Pro	Lys	Glu	Asp	Val	Leu	Ala	Leu	Val	Asn	Asp	Tyr
		35					40						45		

Gly	Ile	Asp	Ile	Val	Gln	Leu	His	Gly	Asp	Glu	Ser	Trp	Gln	Glu	Tyr
	50					55					60				

Gln	Glu	Phe	Leu	Gly	Leu	Pro	Val	Ile	Lys	Arg	Leu	Val	Phe	Pro	Lys
65					70					75					80

Asp	Cys	Asn	Ile	Leu	Leu	Ser	Ala	Ala	Ser	Gln	Lys	Pro	His	Ser	Phe
				85					90					95	

Ile	Pro	Leu	Phe	Asp	Ser	Glu	Ala	Gly	Gly	Thr	Gly	Glu	Leu	Leu	Asp
		100						105					110		

Trp	Asn	Ser	Ile	Ser	Asp	Trp	Val	Gly	Arg	Gln	Glu	Ser	Pro	Glu	Ser
		115					120					125			

Leu	His	Phe	Met	Leu	Ala	Gly	Gly	Leu	Thr	Pro	Glu	Asn	Val	Gly	Asp
	130					135					140				

Ala	Leu	Arg	Leu	Asn	Gly	Val	Ile	Gly	Val	Asp	Val	Ser	Gly	Gly	Val
145					150					155					160

Glu	Thr	Asn	Gly	Val	Lys	Asp	Ser	Asn	Lys	Ile	Ala	Asn	Phe	Val	Lys
				165					170					175	

Asn	Ala	Lys	Lys
			180

<210> 7

<211> 159

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 7

atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgcag 60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgccaata gaaagagaac aattgaccg gttattgca 159

<210> 8

<211> 53

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala
50

<210> 9

<211> 516

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 9

gcaaggaaaa tttcaagtct tgtaaaagct tataaaaata gttcaggcac tccgaaatac 60

ttgggttggcg tgtttcgtaa tcaacctaag gaggatgttt tggctctggt caatgattac 120

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ggcattgata tcgtccaact gcacggagat gagtcgtggc aagaatacca agagttcctc 180
ggtttgccag ttattaaaag actcgtatctt ccaaaagact gcaacatact actcagtgc 240
gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt 300
gaacttttgg attggaactc gatttctgac tgggttgga ggcaagagag ccccgagagc 360
ttacatttta tgtagctgg tggactgacg ccagaaaatg ttggtgatgc gcttagatta 420
aatggcgtaa ttggtgttga tgtaagcgga ggtgtggaga caaatggtgt aaaagactct 480
aacaaaatag caaatctcgt caaaaatgct aagaaa 516

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<210> 10

<211> 172

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly
1           5           10           15

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```

Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp
          20           25           30

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Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His
          35           40           45

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Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val
          50           55           60

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Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala
65           70           75           80

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Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala
          85           90           95

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Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val
          100          105          110

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Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly
          115          120          125

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Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile
          130          135          140

```

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser
 145 150 155 160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
 165 170

<210> 11

<211> 561

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 11
 atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgcag 60
 agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
 gtgccaata gaaagagaac aattgaccog gttattgcaa ggaaaatttc aagtcttgta 180
 aaagcttata aaaatagttc aggcactccg aaataacttg ttggcgtggt tcgtaatcaa 240
 cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300
 ggagatgagt cgtggcaaga ataccaagag ttccctcggt tgccagttat taaaagactc 360
 gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420
 attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480
 tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctggtgga 540
 ctgacgccag aaaatggttg t 561

<210> 12

<211> 187

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
 35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
 50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
 65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
 85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
 100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
 115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
 130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
 145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
 165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly
 180 185

<210> 13

<211> 111

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 13
 gatgcgctta gattaaatgg cgttattggt gttgatgtaa gcggaggtgt ggagacaaat 60

ggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a 111

<210> 14

<211> 37

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly
1 5 10 15

Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val
20 25 30

Lys Asn Ala Lys Lys
35

<210> 15

<211> 612

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> mutation

<222> (22)..(22)

<223> point mutation

<220>

<221> deletion

<222> (612)..(612)

<223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAG
ACTCT

<400> 15

atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgcag 60

agcacagagg cgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgccaata gaaagagaac aattgaccog gttattgcaa ggaaaatttc aagtcttgta 180

aaagcttata aaaatagttc aggcactcog aaatacttgg ttggcgtggt tcgtaatcaa 240

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octaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac 300
ggagatgagt cgtggcaaga ataccaagag ttctctcggtt tgccagttat taaaagactc 360
gtattttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540
ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600
agcggaggtg tg 612

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<210> 16

<211> 204

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

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Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
1           5           10           15

```

```

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
          20           25           30

```

```

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
          35           40           45

```

```

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
          50           55           60

```

```

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65           70           75           80

```

```

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
          85           90           95

```

```

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
          100          105          110

```

```

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
          115          120          125

```

```

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
          130          135          140

```

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
195 200

<210> 17

<211> 36

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> mutation

<222> (1)..(1)

<223> missing sequence before base 1 of SEQ17, corresponding to base 63
7 of wild-type: GAGACAAATGGTGTAAAAGACTCT

<400> 17

aacaaaatag caaatctcgt caaaaatgct aagaaa

36

<210> 18

<211> 12

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
1 5 10

<210> 19

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> first of a pair of peptides (together with peptide C2), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala
1 5 10 15

Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu
20 25 30

Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly
35 40

<210> 20

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> second of a pair of peptides (together with peptide C1), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 20

Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu
1 5 10 15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys
20 25 30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala
35 40 45

Phe Leu
50

<210> 21

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 21

cgatacgaat tcatggacaa ggattgtgaa atgaaacgc

39

<210> 22

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 22

aaaggaattg gcccaaaatg agtgggagtt acaagcaatt gagaa

45

<210> 23

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 23

ctcaatgttc gtgaactctt cctcgagcga gttgaactct tcctc

45

<210> 24

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 24

ctccttctca agttgagcga gctccttctc aagtgtttgt aactc

45

<210> 25

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 25

ggcacttaag aagaagttgg cgcagcttaa gtggaaactg ca

42

<210> 26

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 26

agctggggcat tcttcttctt aagagcttgc agtttccact taagct

46

<210> 27

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 27

aagaagaaga atgccagct taagaagaag ctccaggctg gaagttac

48

<210> 28

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 28

atacgatggt ccagattacg ctgcattttt ataagtcgac tggtc

45

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 29

gaccagtcga cttataaaaa tg

22

<210> 30

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 30

gtaaaagctt ataaaaatag ttcag

25

<210> 31

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 31

gaaatagcct aggatgtctg ttattaattt cacagg 36

<210> 32

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 32

cagacatcct aggcattttc ttagcatttt tgacg 35

<210> 33

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for circular permutation of TRP1

<400> 33

tttataagct tttacaagac ttgaa 25

<210> 34

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 34

gtaacgaatt catggactac aa

22

<210> 35

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 35

cattttgggc caattccttt tccagtgcct gaccactttc gtctttgtag tccatgaatt

60

cgttac

66

<210> 36

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 36

caactttctt ttaagtgcct gacctgatcc agatccaccg ttaacacctg aacctgatcc

60

ggcc

64

<210> 37

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS316-C1/2CUP1

<400> 37

gtaatctgga acatcgtatg ggtaacttcc agcctggagc ttc 43

<210> 38

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for homologous recombination

<400> 38

gactctaaca aaatagcaaa ttctgtcaaa aatgctaaga aatagagggc cgcacatcatgt 60

aattag 66

<210> 39

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for homologous recombination

<400> 39

aacttttcacc aatggaccag aactacctgt gaaattaata acagacattt tgagatccgg 60

gtttt 65

<210> 40

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 40

gcctgatcca gatccgcctt ctggtgattc atcatcttca

40

<210> 41

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 41

ggcggatctg gatcaggcaa gagaacaatt gaccgggta

40

<210> 42

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 42

gcctgatcca gatccgccta taaaaggat tccgacacca

40

<210> 43

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 43

gcctgatcca gatccgcctg caataaccgg gtcaattgt

39

<210> 44

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 44

ggcggatctg gatcaggcgc aaggaaaatt tcaagtcttg

40

<210> 45

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 45

gcctgatcca gatccgccac caacattttc tggcgtcagt cc

42

<210> 46

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 46

ggcggatctg gatcaggcga tgcgcttaga ttaaattggc

39

<210> 47

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ntrp fusions

<400> 47

gcctgatcca gatccgccca cacctccgct tacatcaac

39

<210> 48

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Ctrp fusions

<400> 48

ggcggatctg gatcaggcaa caaaatag

28

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 49

agcaggatcc cattaccgac atttg

25

<210> 50

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 50

cctaggttga gatctcttga attcgttaca gtttgttttt c

41

<210> 51

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for pRS315CUP1/ pRS316CUP1

<400> 51

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68

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